

36555

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in 40  
4/10

Cancel

5	10	15	20
MetSerTyrAsnLeu	LeuGlyPheLeuGln	ArgSerSerAsnPhe	GlnCysGlnLysLeu
25	30	35	40
LeuTrpGlnLeuAsn	GlyArgLeuGluTyr	CysLeuLysAspArg	MetAsnPheAspIle
45	50	55	60
ProGluGluIleLys	GlnLeuGlnGlnPhe	GlnLysGluAspAla	AlaLeuThrIleTyr
65	70	75	80
GluMetLeuGlnAsn	IlePheAlaIlePhe	ArgGlnAspSerSer	SerThrGlyTrpAsn
85	90	95	100
GluThrIleValGlu	AsnLeuLeuAlaAsn	ValTyrHisGlnIle	AsnHisLeuLysThr
105	110	115	120
ValLeuGluGluLys	LeuGluLysGluAsp	PheThrArgGlyLys	LeuMetSerSerLeu
125	130	135	140
HisLeuLysArgTyr	TyrGlyArgIleLeu	HisTyrLeuLysAla	LysGluTyrSerHis
145	150	155	160
CysAlaTrpThrIle	ValArgValGluIle	LeuAgAsnPheTyr	PheIleAsnArgLeu
165	170	175	180
ThrGlyTyrLeuArg	Asn---		

FIG. 1

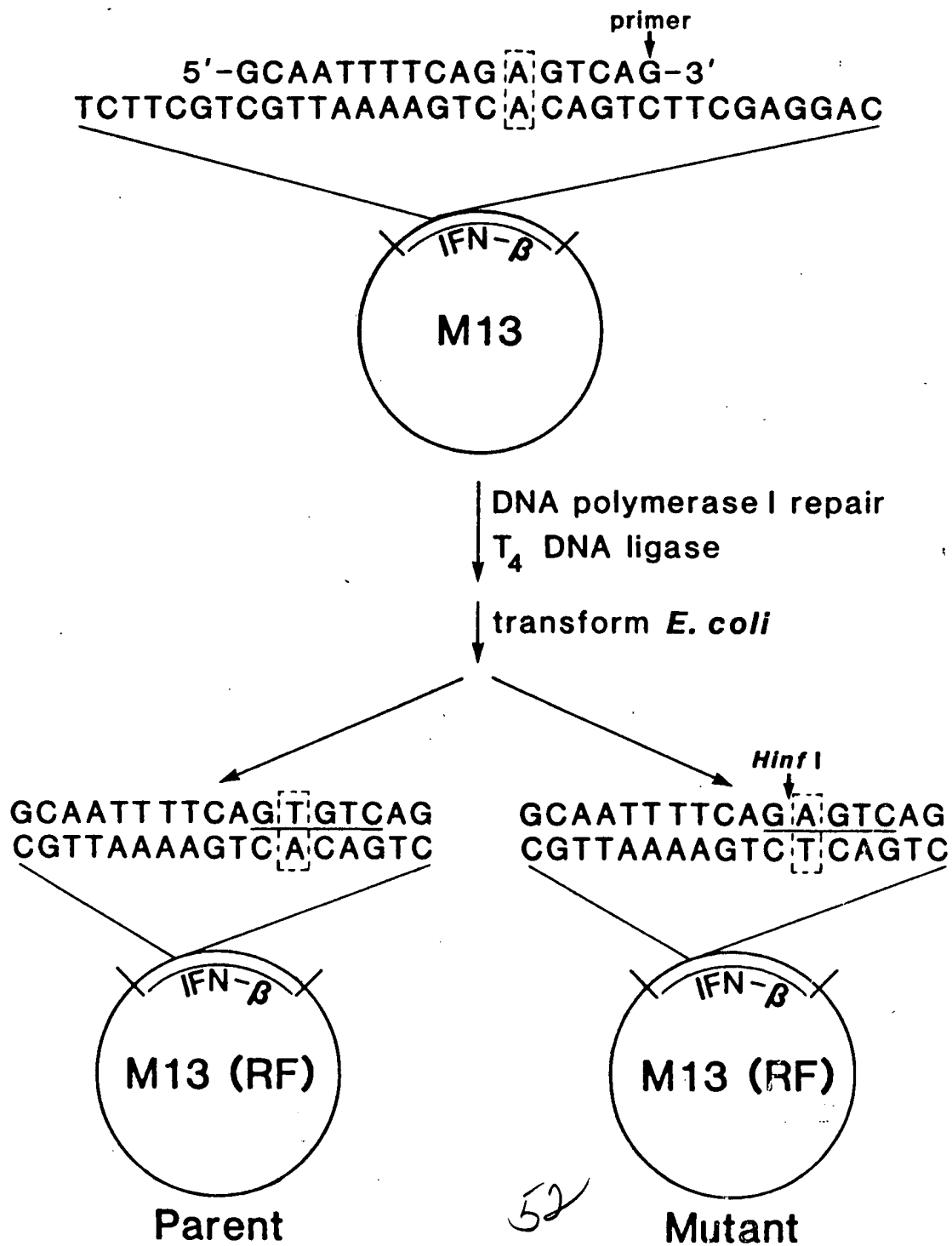


FIG. 2

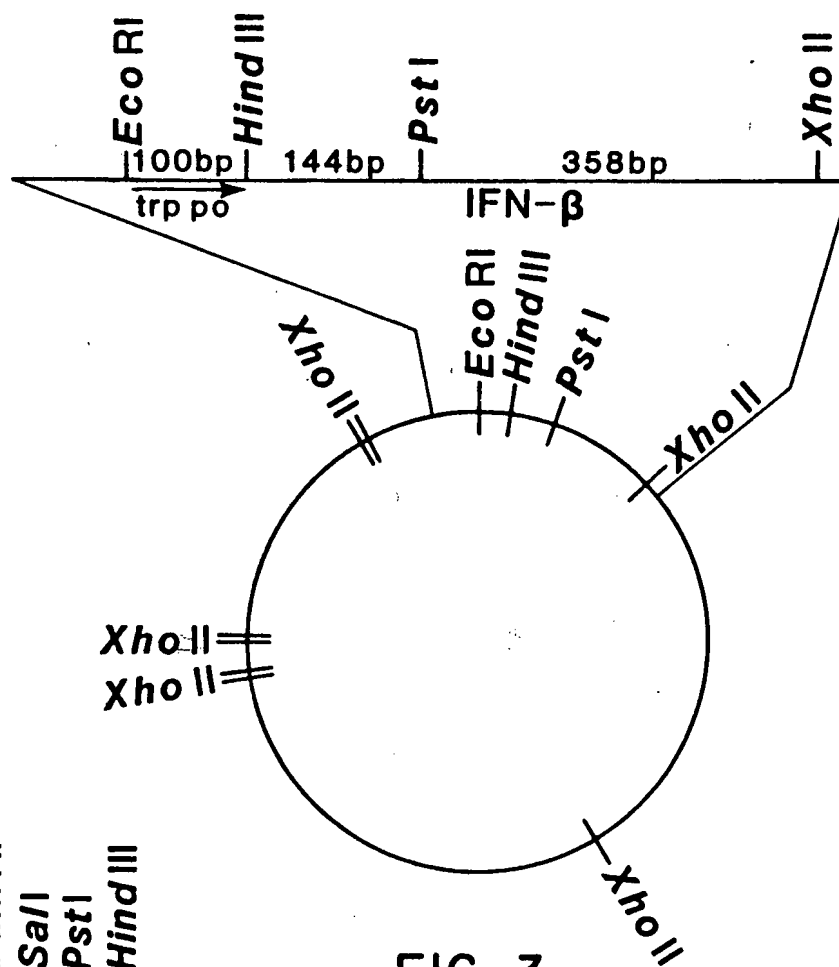


FIG. 3

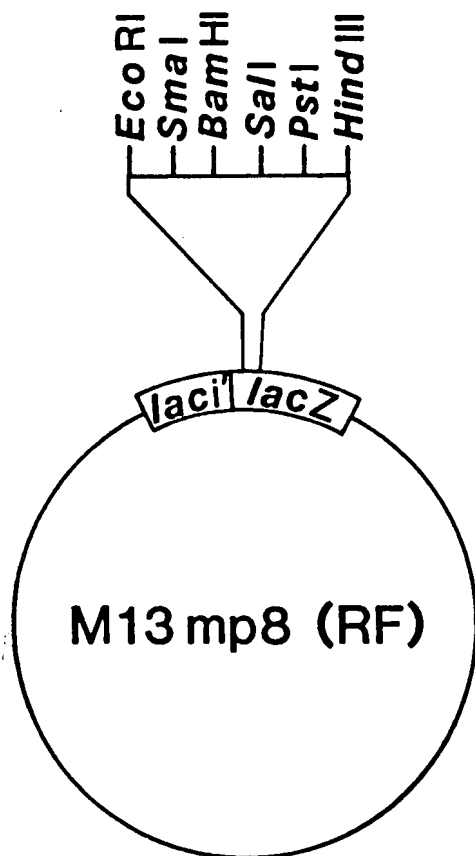


FIG. 4

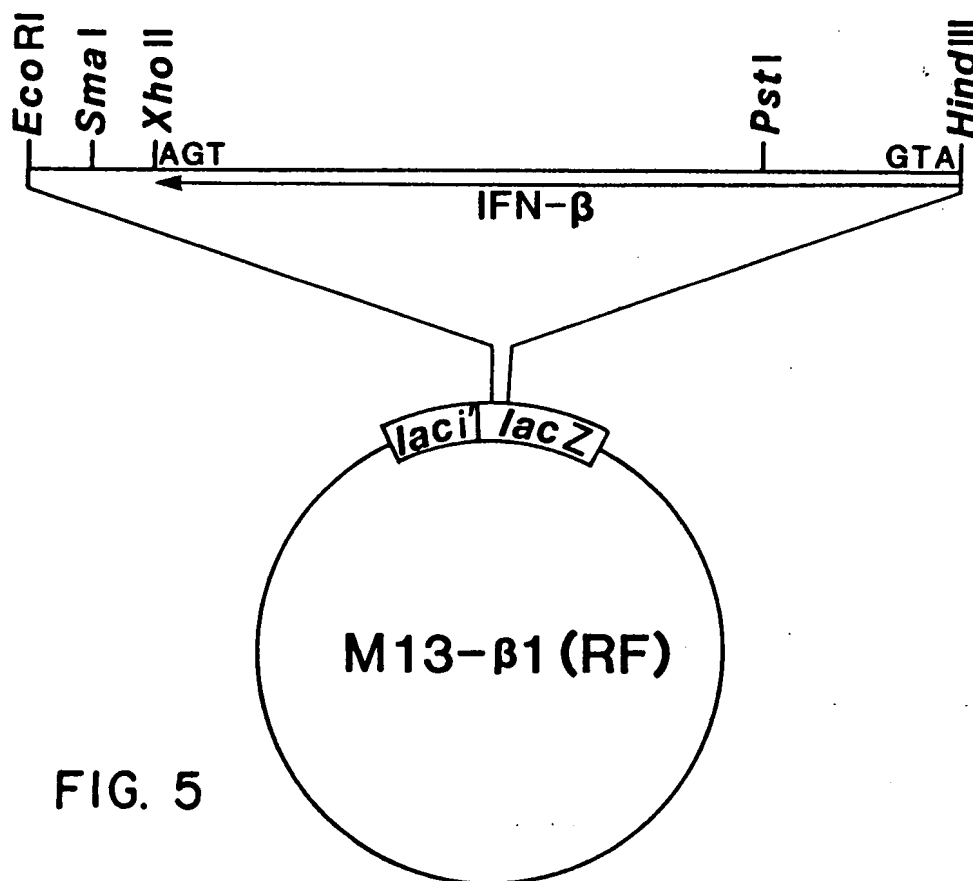


FIG. 5

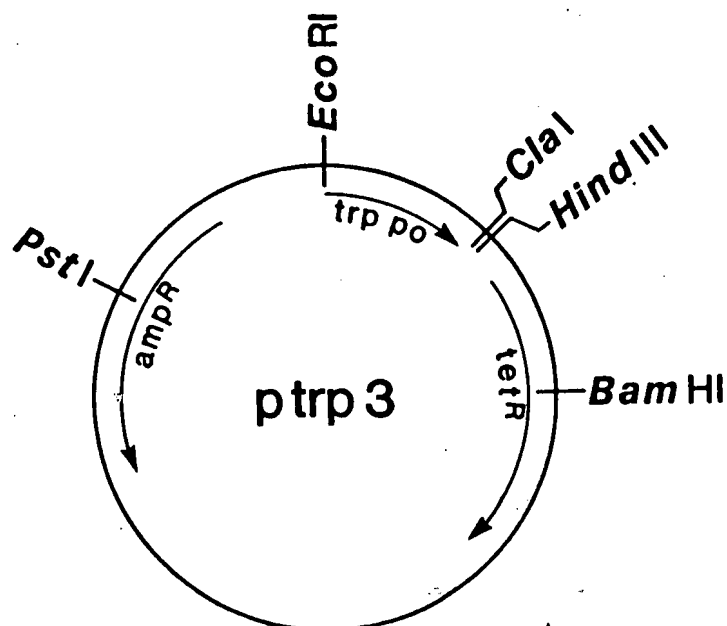


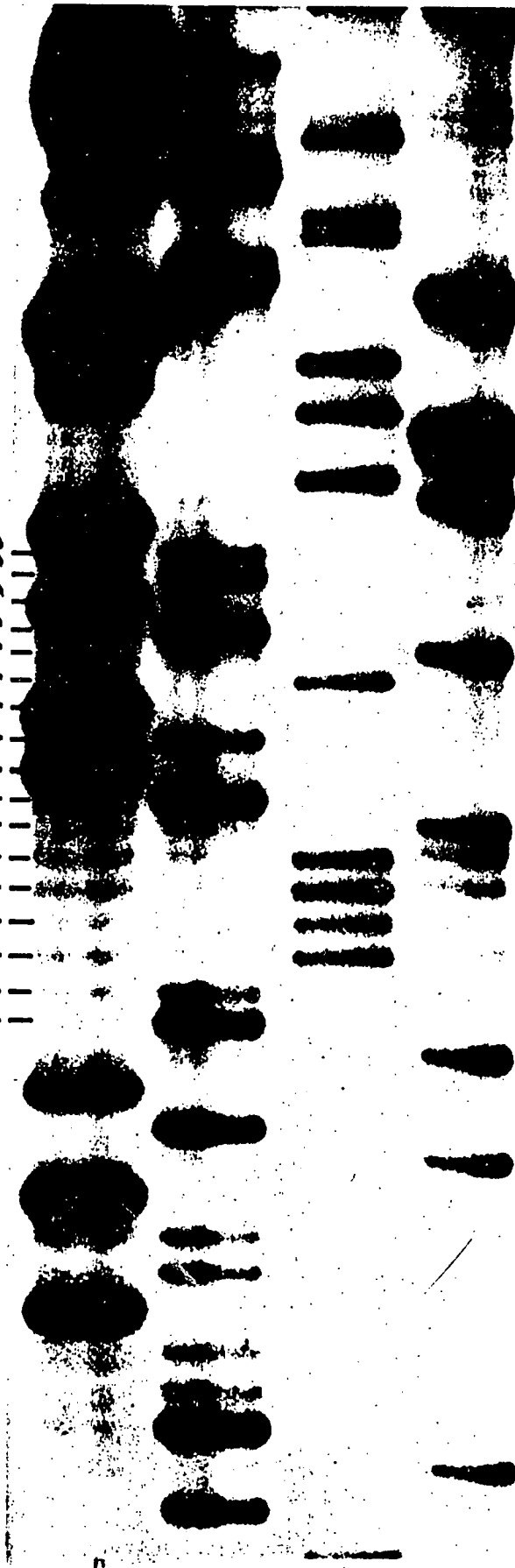
FIG. 7

54

G A T C

FIG. 6

A  
A  
G  
A  
C  
T  
G  
**A**  
G  
A  
C  
T  
T  
T  
T  
A  
A



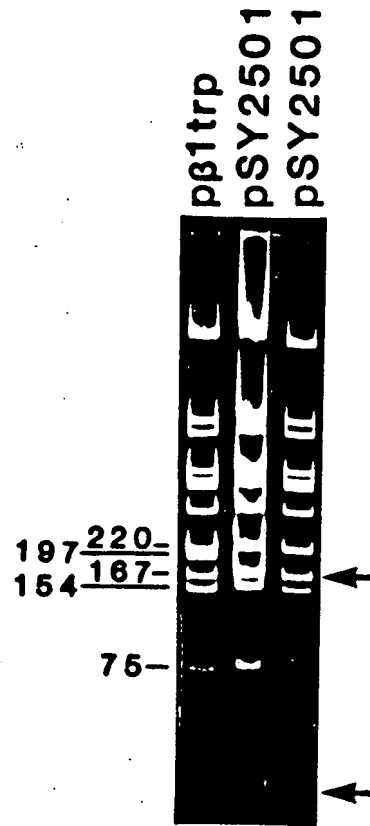


FIG. 8a

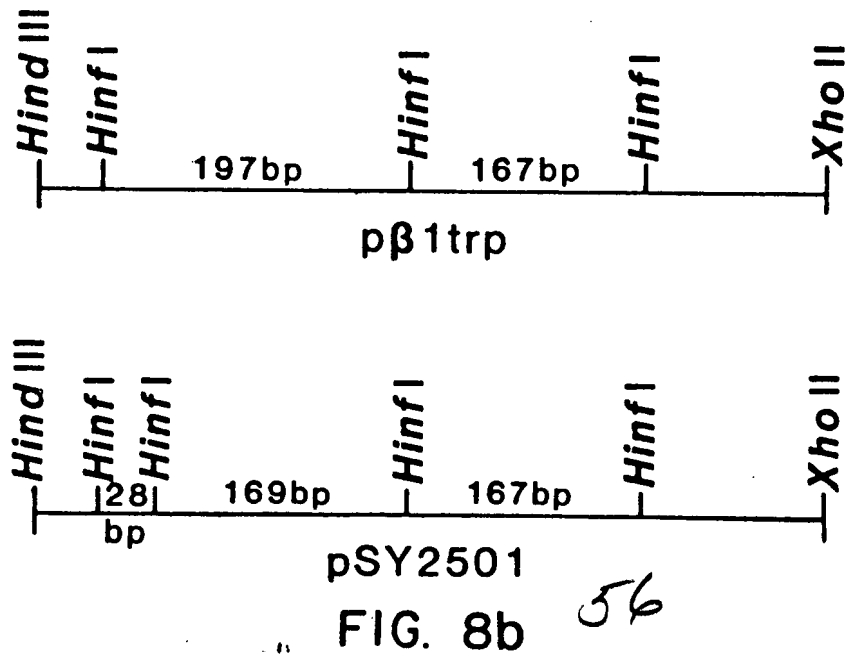


FIG. 8b

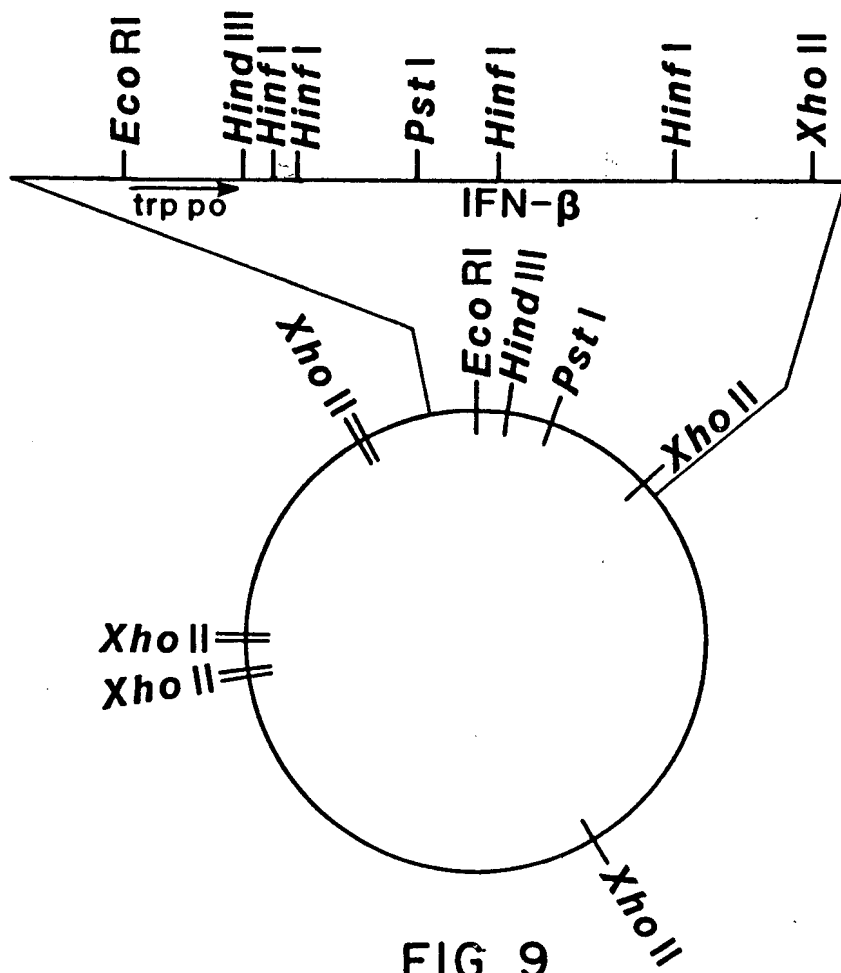


FIG. 9

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IFN-B CYS TO SER CHANGE AT AMINO ACID 17

1  
ATG AGC TAC AAC TTG CTT GGA TTC CTA CAA AGA AGC AGC AAT TTT CAG <sup>17</sup>AGT CAG AAG CTC  
met ser tyr asn leu leu gly phe leu gln arg ser ser asn phe gln ser gln lys leu

61  
CTG TGG CAA TTG AAT GGG AGG CTT GAA TAT TGC CTC AAG GAC AGG ATG AAC TTT GAC ATC  
leu trp gln leu asn gly arg leu glu tyr cys leu lys asp arg met asn phe asp ile

121  
CCT GAG GAG ATT AAG CAG CTG CAG CAG TTC CAG AAG GAG GAC GCC GCA TTG ACC ATC TAT  
pro glu glu ile lys gln leu gln gln phe gln lys glu asp ala ala leu thr ile tyr

181  
GAG ATG CTC CAG AAC ATC TTT GCT ATT TTC AGA CAA GAT TCA TCT AGC ACT GGC TGG AAT  
glu met leu gln asn ile phe ala ile phe arg gln asp ser ser ser thr gly trp asn

241  
GAG ACT ATT GTT GAG AAC CTC CTG GCT AAT GTC TAT CAT CAG ATA AAC CAT CTG AAG ACA  
glu thr ile val glu asn leu leu ala asn val tyr his gln ile asn his leu lys thr

301  
GTC CTG GAA GAA AAA CTG GAG AAA GAA GAT TTC ACC AGG GGA AAA CTC ATG AGC AGT CTG  
val leu glu glu lys leu glu lys glu asp phe thr arg gly lys leu met ser ser leu

361  
CAC CTG AAA AGA TAT TAT GGG AGG ATT CTG CAT TAC CTG AAG GCC AAG GAG TAC AGT CAC  
his leu lys arg tyr tyr gly arg ile leu his tyr leu lys ala lys glu tyr ser his

421  
TGT GCC TGG ACC ATA GTC AGA GTG GAA ATC CTA AGG AAC TTT TAC TTC ATT AAC AGA CTT  
cys ala trp thr ile val arg val glu ile leu arg asn phe tyr phe ile asn arg leu

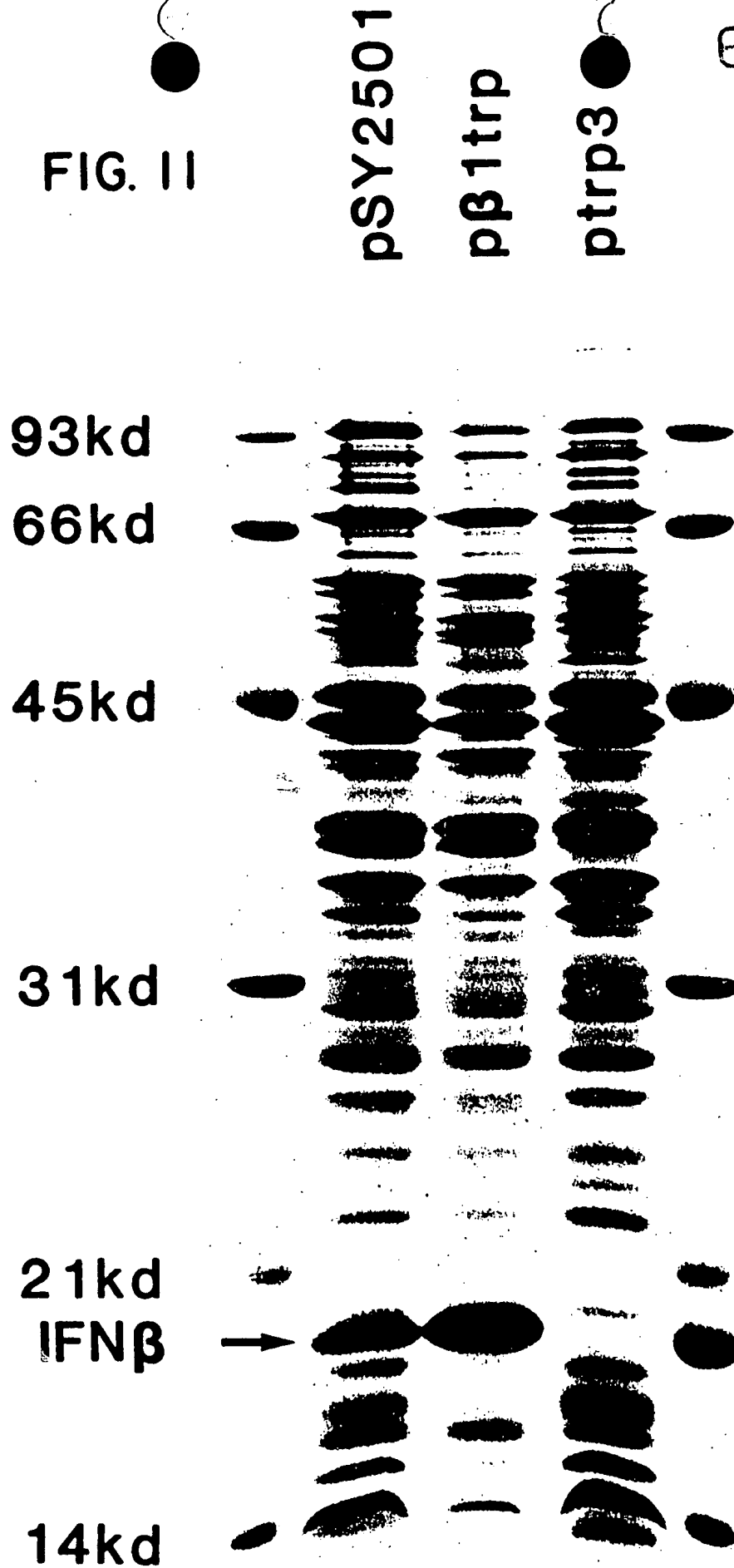
481  
ACA GGT TAC CTC CGA AAC TGA AGA TC  
thr gly tyr leu arg asn \*\*\*

FIG. 10

58



FIG. II



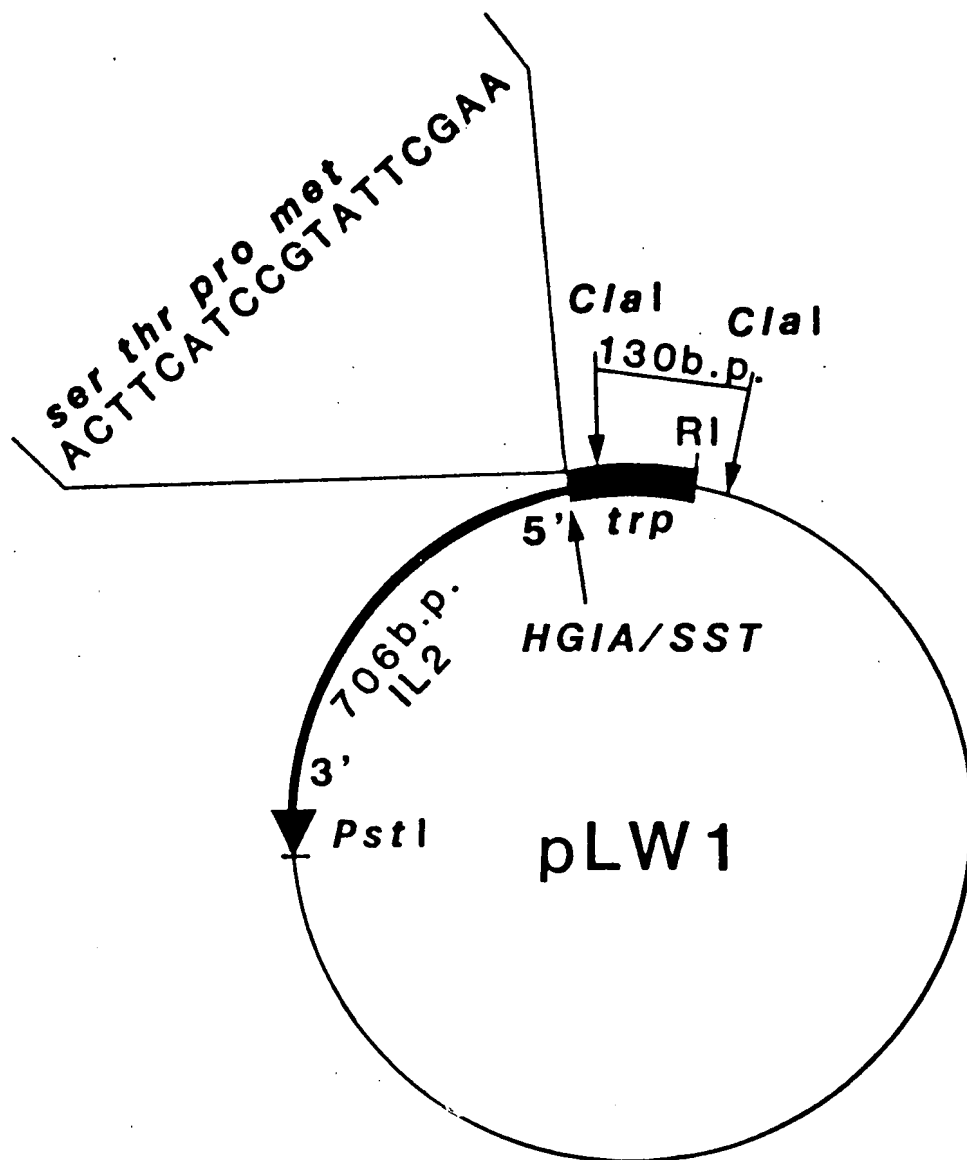


FIG. 12

1. 1000-000  
D. 1. 1. 1. 1. 1.  
11. 11. 11.

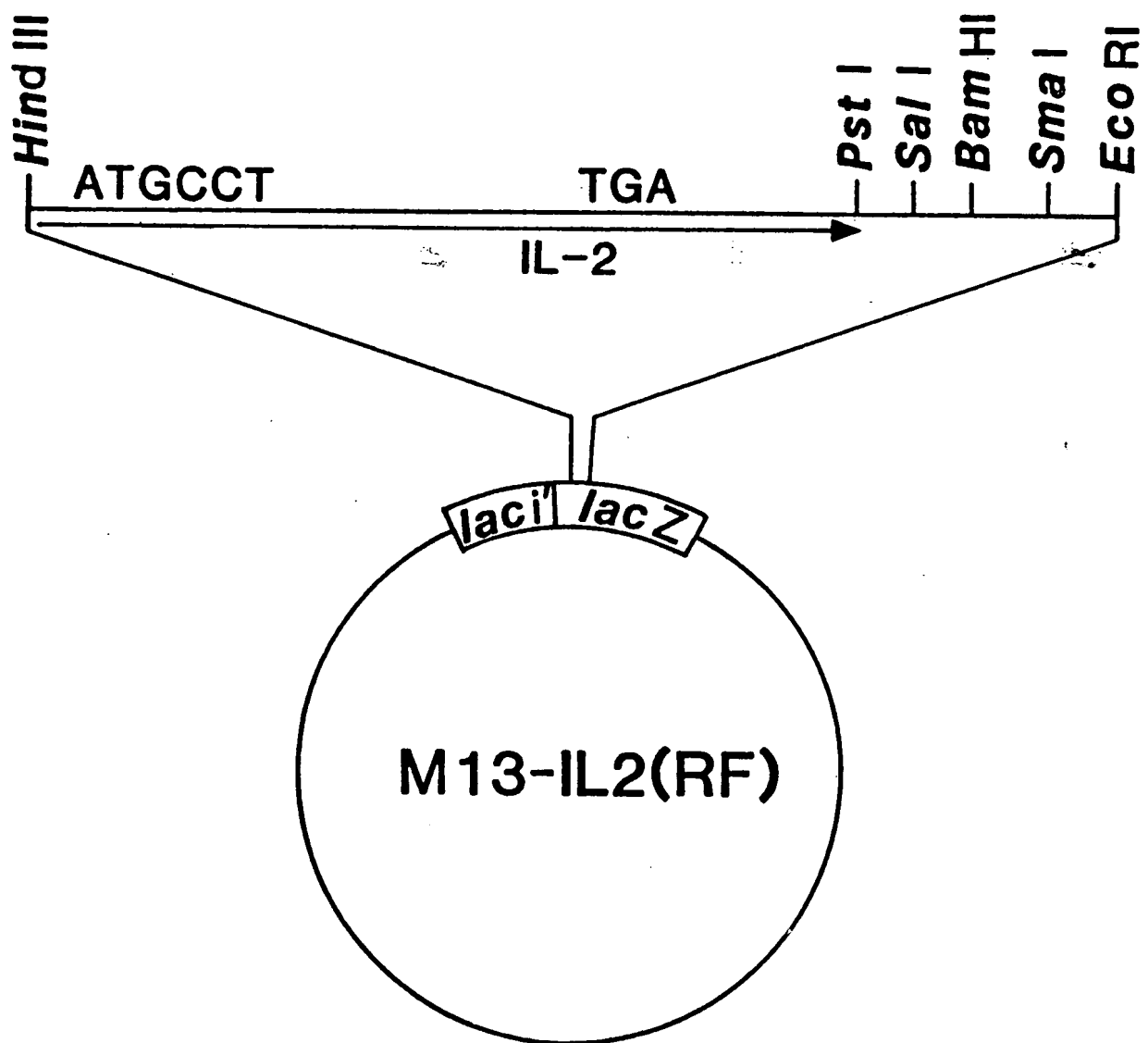


FIG. 13

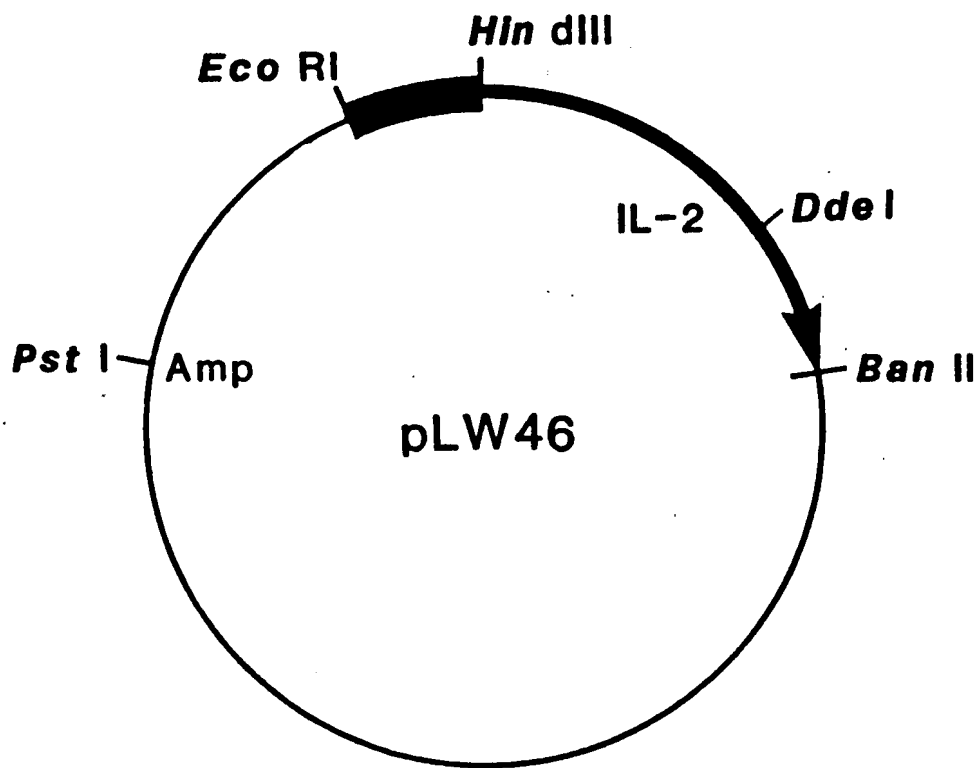


FIG. 14

10	20	30	40	50	60
ATGCCTACTT	CAAGTTCTAC	AAAGAAAACA	CAGCTACAAC	TGGAGCATTT	ACTGCTGGAT
70	80	90	100	110	120
TTACAGATGA	TTTTGAATGG	AATTAATAAT	TACAAGAATC	CCAAACTCAC	CAGGATGCTC
130	140	150	160	170	180
ACATTTAAGT	TTTACATGCC	CAAGAAGGCC	ACAGAACTGA	AACATCTTCA	GTGTCTAGAA
190	200	210	220	230	240
GAAGAACTCA	AACCTCTGGA	GGAAGTGCTA	AATTTAGCTC	AAAGCAAAAA	CTTTCACCTA
250	260	270	280	290	300
AGACCCAGGG	ACTTAATCAG	CAATATCAAC	GTAATAGTTC	TGGAACTAAA	GGGATCTGAA
310	320	330	340	350	360
ACAACATTCA	TGTGTGAATA	TGCTGATGAG	ACAGCAACCA	TTGTAGAATT	TCTGAACAGA
370	380	390	400	410	420
TGGATTACCT	TTTCTCAGAG	CATCATCTCA	ACACTGACTT	GA	

FIG. 15a

5	10	15	20
MetProThrSerSer	SerThrLysLysThr	GlnLeuGlnLeuGlu	HisLeuLeuLeuAsp
25	30	35	40
LeuGlnMetIleLeu	AsnGlyIleAsnAsn	TyrLysAsnProLys	LeuThrArgMetLeu
45	50	55	60
ThrPheLysPheTyr	MetProLysLysAla	ThrGluLeuLysHis	LeuGlnCysLeuGlu
65	70	75	80
GluGluLeuLysPro	LeuGluGluValLeu	AsnLeuAlaGlnSer	LysAsnPheHisLeu
85	90	95	100
ArgProArgAspLeu	IleSerAsnIleAsn	ValIleValLeuGlu	LeuLysGlySerGlu
105	110	115	120
ThrThrPheMetCys	GluTyrAlaAspGlu	ThrAlaThrIleVal	GluPheLeuAsnArg
125	130	135	140
TrpIleThrPheSer	GlnSerIleIleSer	ThrLeuThr---	

FIG. 15b

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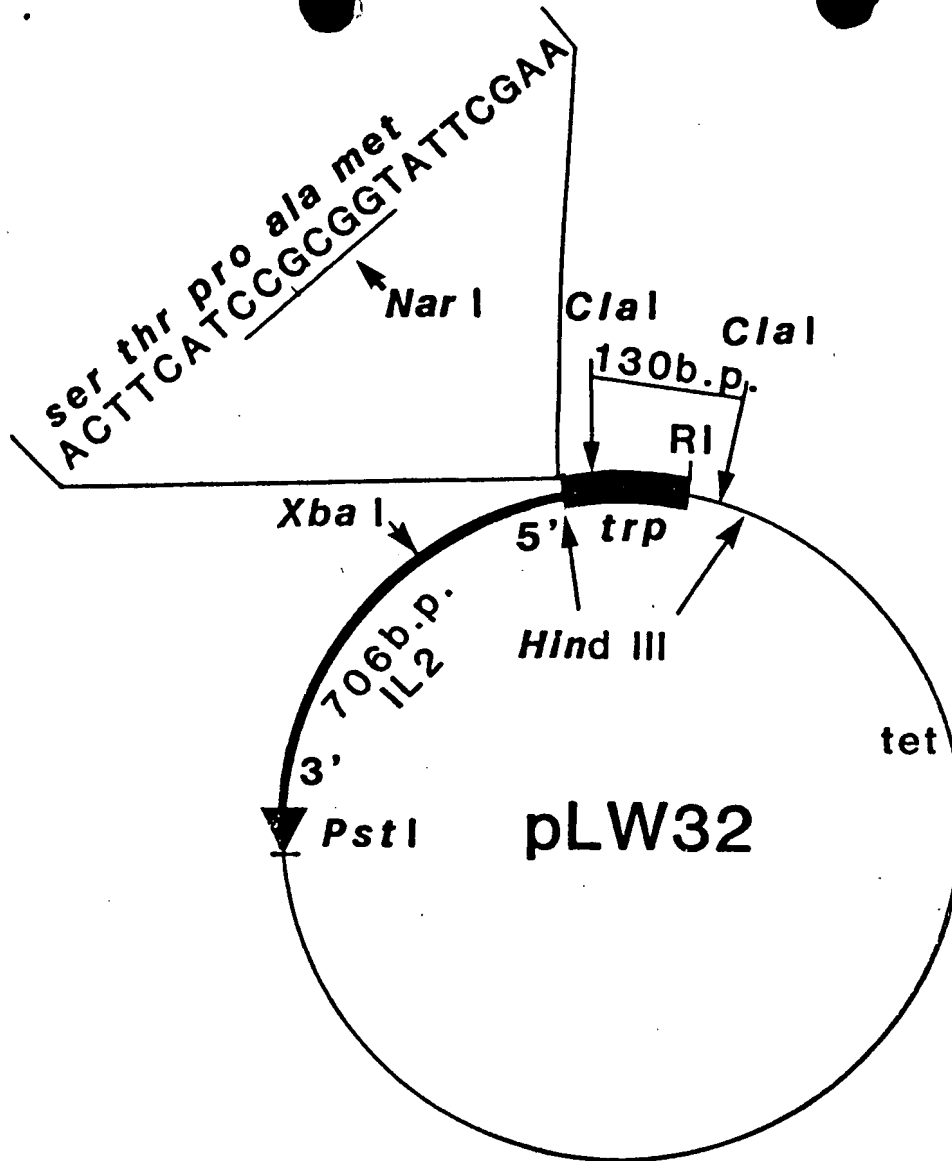


FIGURE 16

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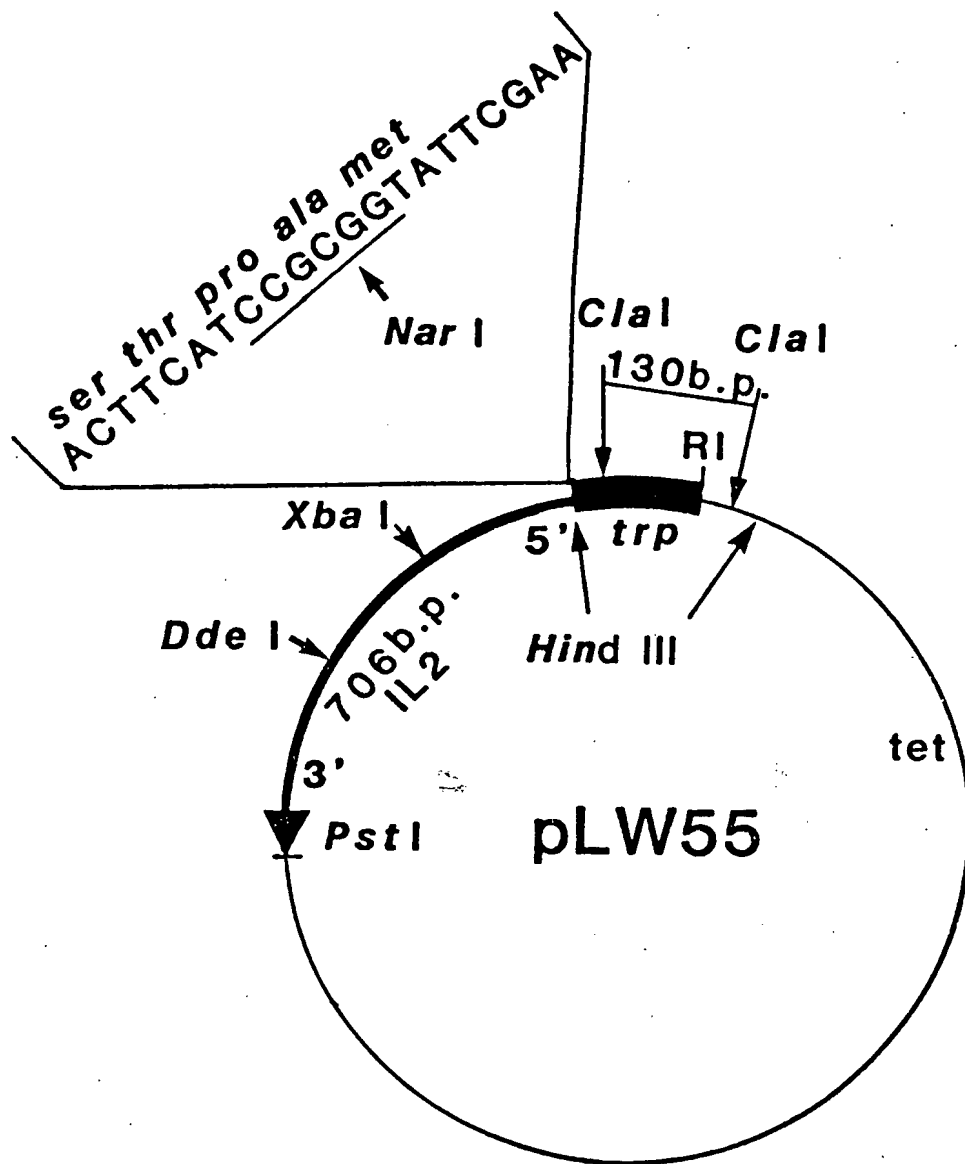


FIGURE 17